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SEQUENCE LISTING

SEQ ID NO: 1

SEQUENCE TYPE: Amino acid

SEQUENCE LENGTH: 9

TOPOLOGY: Linear

MOLECULE TYPE: Peptide

SEQUENCE

Xxx Glu Thr Ile Asn Xxx His Phe Lys

1 5 9

SEQ ID NO: 2

SEQUENCE TYPE: Amino acid

SEQUENCE LENGTH: 7

TOPOLOGY: Linear

MOLECULE TYPE: Peptide

SEQUENCE

Xxx Gln Xxx Ala Phe Thr Lys

1 5 7

SEQ ID NO: 3

SEQUENCE TYPE: Amino acid

SEQUENCE LENGTH: 19

TOPOLOGY: Linear

MOLECULE TYPE: Peptide

SEQUENCE

Val Glu Xxx Val Asp Phe Thr Asn His Leu Glu Asp Thr Xxx Xxx Asn

1 5 10 15

Ile Asn Lys

19

SEQ ID NO: 4

SEQUENCE TYPE: Amino acid

SEQUENCE LENGTH: 17

TOPOLOGY: Linear

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MOLECULE TYPE: Peptide

SEQUENCE

Xxx Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala Xxx Ala

1

5

10

15

Ala Xxx Gly

17

SEQ ID NO: 5

SEQUENCE TYPE: Amino acid

SEQUENCE LENGTH: 9

TOPOLOGY: Linear

MOLECULE TYPE: Peptide

SEQUENCE

Xxx Tyr Leu Arg Ala Leu Gly Leu Lys

1

5

9

SEQ ID NO: 6

SEQUENCE TYPE: Amino acid

SEQUENCE LENGTH: 20

TOPOLOGY: Linear

MOLECULE TYPE: Peptide

SEQUENCE

Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg

1

5

10

15

Met Xxx Gly Lys

20

SEQ ID NO: 7

SEQUENCE TYPE: Amino acid

SEQUENCE LENGTH: 5

TOPOLOGY: Linear

MOLECULE TYPE: Peptide

SEQUENCE

Leu Tyr Asp Ala Lys

1

5

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SEQ ID NO: 8  
SEQUENCE TYPE: Amino acid  
SEQUENCE LENGTH: 5  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
SEQUENCE  
Asn Tyr Glu Met Lys  
1 5

SEQ ID NO: 9  
SEQUENCE TYPE: Amino acid  
SEQUENCE LENGTH: 10  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
SEQUENCE  
Ala Val Ala Met Met His Gln Xxx Arg Lys  
1 5 10

SEQ ID NO: 10  
SEQUENCE TYPE: Nucleic acid  
SEQUENCE LENGTH: 38  
STRANDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Synthetic DNA  
FEATURES: corresponding to amino acid sequence of SEQ ID NO: 3; I is  
inosine.  
SEQUENCE  
GTIGARIIIIG TIGAYTTYAC IAAAYCAYYTI GARGAYAC 38

SEQ ID NO: 11  
SEQUENCE TYPE: Nucleic acid  
SEQUENCE LENGTH: 32  
STRANDNESS: Single  
TOPOLOGY: Linear

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MOLECULE TYPE: Synthetic DNA

FEATURES: corresponding to amino acid sequence of SEQ ID NO: 4; I is inosine.

SEQUENCE

TACATCGAIG TIACIGARGA RGGIACNGAR GC 32

SEQ ID NO: 12

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 37

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

FEATURES: Oligomer attached to 3'-RACE kit (Gibco BRL).

SEQUENCE

GGCCACGCGT CGACTAGTAC TTTTTTTTTT TTTTTTT 34

SEQ ID NO: 13

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 20

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

SEQUENCE

ATGTTGTGGG GACTGCTATA 20

SEQ ID NO: 14

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 23

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

SEQUENCE

CAAGGCGAAT GACCTCTAAG TAT 23

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SEQ ID NO: 15  
SEQUENCE TYPE: Nucleic acid  
SEQUENCE LENGTH: 21  
STRANDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Synthetic DNA  
SEQUENCE  
CCCCGAAGCA ATCCCAGAGA G 21

SEQ ID NO: 16  
SEQUENCE TYPE: Nucleic acid  
SEQUENCE LENGTH: 21  
STRANDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Synthetic DNA  
SEQUENCE  
CTCAGGCAGC AGAACGTACA T 21

SEQ ID NO: 17  
SEQUENCE TYPE: Nucleic acid  
SEQUENCE LENGTH: 21  
STRANDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Synthetic DNA  
SEQUENCE  
GGCGACGACT CCTGGAGCCC G 21

SEQ ID NO: 18  
SEQUENCE TYPE: Nucleic acid  
SEQUENCE LENGTH: 22  
STRANDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Synthetic DNA  
SEQUENCE  
GACACCAGAC CAACTGGTAA TG 22

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SEQ ID NO: 19

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 36

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

SEQUENCE

CATCCGGGAG ATGTACAGCC GGCCGCCAGA GGCAAT

36

SEQ ID NO: 20

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 21

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

SEQUENCE

GCTGTGGCCA TGATGCACCA G

21

SEQ ID NO: 21

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 24

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

SEQUENCE

TACCTGCGGG CCCTGGGCCT GAAG

24

SEQ ID NO: 22

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 51

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

SEQUENCE

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CATCCGGGAG ATGTACAGCC GGCCGCCAGA GGCAATGCCA GACAGGTCAG C 51

SEQ ID NO: 23

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 17

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

SEQUENCE

GTTTTCCCAG TCACGAC 17

SEQ ID NO: 24

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 17

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

SEQUENCE

CAGGAAACAG CTATGAC 17

SEQ ID NO: 25

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 20

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

SEQUENCE

AATTATGGCC CACACCAAGTG 20

SEQ ID NO: 26

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 20

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

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## SEQUENCE

ACTAGCCGCT ACAGTCAACA

20

SEQ ID NO: 27

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 21

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

## SEQUENCE

TTGCCACTTG CCTTTGAAGT A

21

SEQ ID NO: 28

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 21

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

## SEQUENCE

CTGATGCATC ATGGCGACTG C

21

SEQ ID NO: 29

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 21

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

## SEQUENCE

AGCATTACC AGCACCATTA C

21

SEQUENCE ID NO: 30

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 1950

STRANDNESS: Double

TOPOLOGY: Linear



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MOLECULE TYPE: complimentary DNA (cDNA)

ORIGINAL SOURCE: Human

IMMEDIATE SOURCE: A431

FEATURE: DNA coding for human megakaryocyte differentiation factor  
SEQUENCE

GGCACGAGAG GAACTGAAGC CCAGCTGTGA AGGCCGCAGA CTGCAGTGAG 50

AGGAGGCTGC ACTCCATTTT GCA ATG GCC TCC CTT GCT GCA GCA AAT 97

Met Ala Ser Leu Ala Ala Ala Asn

1

5

GCA GAG TTT TGC TTC AAC CTG TTC AGA GAG ATG GAT GAC AAT CAA 142

Ala Glu Phe Cys Phe Asn Leu Phe Arg Glu Met Asp Asp Asn Gln

10

15

20

GGA AAT GGA AAT GTG TTC TTT TCC TCT CTG AGC CTC TTC GCT GCC 187

Gly Asn Gly Asn Val Phe Phe Ser Ser Leu Ser Leu Phe Ala Ala

25

30

35

CTG GCC CTG GTC CGC TTG GGC GCT CAA GAT GAC TCC CTC TCT CAG 232

Leu Ala Leu Val Arg Leu Gly Ala Gln Asp Asp Ser Leu Ser Gln

40

45

50

ATT GAT AAG TTG CTT CAT GTT AAC ACT GCC TCA GGA TAT GGA AAC 277

Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser Gly Tyr Gly Asn

55

60

65

TCT TCT AAT AGT CAG TCA GGG CTC CAG TCT CAA CTG AAA AGA GTT 322

Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu Lys Arg Val

70

75

80

TTT TCT GAT ATA AAT GCA TCC CAC AAG GAT TAT GAT CTC AGC ATT 367

Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu Ser Ile

85

90

95

GTG AAT GGG CTT TTT GCT GAA AAA GTG TAT GGC TTT CAT AAG GAC 412

Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys Asp

100

105

110

TAC ATT GAG TGT GCC GAA AAA TTA TAC GAT GCC AAA GTG GAG CGA 457

Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg

115

120

125

GTT GAC TTT ACG AAT CAT TTA GAA GAC ACT AGA CGT AAT ATT AAT 502

Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn

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130	135	140	
AAG TGG GTT GAA AAT GAA ACA CAT GGC AAA ATC AAG AAC GTG ATT	547		
Lys Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile			
145	150	155	
GGT GAA GGT GGC ATA AGC TCA TCT GCT GTA ATG GTG CTG GTG AAT	592		
Gly Glu Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn			
160	165	170	
GCT GTG TAC TTC AAA GGC AAG TGG CAA TCA GCC TTC ACC AAG AGC	637		
Ala Val Tyr Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser			
175	180	185	
GAA ACC ATA AAT TGC CAT TTC AAA TCT CCC AAG TGC TCT GGG AAG	682		
Glu Thr Ile Asn Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys			
190	195	200	
GCA GTC GCC ATG ATG CAT CAG GAA CGG AAG TTC AAT TTG TCT GTT	727		
Ala Val Ala Met Met His Gln Glu Arg Lys Phe Asn Leu Ser Val			
205	210	215	
ATT GAG GAC CCA TCA ATG AAG ATT CTT GAG CTC AGA TAC AAT GGT	772	Ile Glu	
Asp Pro Ser Met Lys Ile Leu Glu Leu Arg Tyr Asn Gly			
220	225	230	
GGC ATA AAC ATG TAC GTT CTG CTG CCT GAG AAT GAC CTC TCT GAA	817		
Gly Ile Asn Met Tyr Val Leu Leu Pro Glu Asn Asp Leu Ser Glu			
235	240	245	
ATT GAA AAC AAA CTG ACC TTT CAG AAT CTA ATG GAA TGG ACC AAT	862		
Ile Glu Asn Lys Leu Thr Phe Gln Asn Leu Met Glu Trp Thr Asn			
250	255	260	
CCA AGG CGA ATG ACC TCT AAG TAT GTT GAG GTA TTT TTT CCT CAG	907		
Pro Arg Arg Met Thr Ser Lys Tyr Val Glu Val Phe Phe Pro Gln			
265	270	275	
TTC AAG ATA GAG AAG AAT TAT GAA ATG AAA CAA TAT TTG AGA GCC	952		
Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys Gln Tyr Leu Arg Ala			
280	285	290	
CTA GGG CTG AAA GAT ATC TTT GAT GAA TCC AAA GCA GAT CTC TCT	997		
Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys Ala Asp Leu Ser			
295	300	305	
GGG ATT GCT TCG GGG GGT CGT CTG TAT ATA TCA AGG ATG ATG CAC	1042		

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Gly	Ile	Ala	Ser	Gly	Gly	Arg	Leu	Tyr	Ile	Ser	Arg	Met	Met	His	
310						315					320				
AAA	TCT	TAC	ATA	GAG	GTC	ACT	GAG	GAG	GGC	ACC	GAG	GCT	ACT	GCT	1087
Lys	Ser	Tyr	Ile	Glu	Val	Thr	Glu	Glu	Gly	Thr	Glu	Ala	Thr	Ala	
325						330					335				
GCC	ACA	GGA	AGT	AAT	ATT	GTA	GAA	AAG	CAA	CTC	CCT	CAG	TCC	ACG	1132
Ala	Thr	Gly	Ser	Asn	Ile	Val	Glu	Lys	Gln	Leu	Pro	Gln	Ser	Thr	
340						345					350				
CTG	TTT	AGA	GCT	GAC	CAC	CCA	TTC	CTA	TTT	GTT	ATC	AGG	AAG	GAT	1177
Leu	Phe	Arg	Ala	Asp	His	Pro	Phe	Leu	Phe	Val	Ile	Arg	Lys	Asp	
355						360					365				
GAC	ATC	ATC	TTA	TTC	AGT	GGC	AAA	GTT	TCT	TGC	CCT	TGA			1216
Asp	Ile	Ile	Leu	Phe	Ser	Gly	Lys	Val	Ser	Cys	Pro	...			
370						375					380				
AAATCCAATT	GGTTTCTGTT	ATAGCAGTCC	CCACAACATC	AAAGAACCAC											1266
CACAAGTCAA	TAGATTTGAG	TTTAATTGGA	AAAATGTGGT	GTTTCCTTTG											1316
AGTTTATTTT	TTCTTAACAT	TGGTCAGCAG	ATGACACTGG	TGACTTGACC											1366
CTTCCTAGAC	ACCTGGTTGA	TTGTCCTGAT	CCCTGCTCTT	AGCATTCTAC											1416
CACCATGTGT	CTCACCCATT	TCTAATTTCA	TTGTCTTTCT	TCCCACGCTC											1466
ATTTCTATCA	TTCTCCCCCA	TGACCCGTCT	GGAAATTATG	GAGAGTGCTC											1516
AACTGGTAAG	GAGAACGTAG	AAGTAGCCCT	AGGGATCCTT	TTTGAAACTC											1566
TACAGTTATC	GCAGATATTC	TAGCTTCATT	GTAAGCAATC	TAGGAAATAA											1616
GCCCTGCTGC	TTTCTAGAAA	TAAGTGTGAA	GGATAAATTT	TCTTTGTTGA											1666
CCTATGAAGA	TTTTAGAGTT	TACCTTCATA	TGTTTGATTT	TAAATCAGTG											1716
TATAATCTAG	ATGGTAAAAA	ATGTGAAATT	GGGATTAGGG	ACCAACCAAA											1766
ATATTTTATT	AATGCTTTCA	ATTGACAAAT	TTTGGTCTTT	CTTTGATAAG											1816
ACAATATGTA	CATAGTTTTT	TCAAATATTA	AAGATCTTTT	AACTGTTGGC											1866
AGTTGTTATC	TACAGAATCA	TATCTCATAT	GCTGTGTAGT	TTATAAGTTT											1916
TTTCTCTATT	TATCAGAATA	AAGAAATACA	ACAT												1950

SEQ ID NO: 31

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 20

STRANDNESS: Single

TOPOLOGY: Linear

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MOLECULE TYPE: Synthetic DNA

ORIGINAL SOURCE: Human

FEATURES: 5'-non-translation region

SEQUENCE

AACTGAAGCC CAGCTGTGAA

20

SEQ ID NO: 32

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 37

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

SEQUENCE

CTCGAATTCG CGATGGCCTC CCTTGCTGCA GCAAATG

37

SEQ ID NO: 33

SEQUENCE TYPE: Nucleic acid

SEQUENCE LENGTH: 49

STRANDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Synthetic DNA

SEQUENCE

GGGAATTCGC GGCCGCGTGG TGGTTCTTTG ATGTTGTGGG GACTGCTAT

49